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Performance of the RapidHIT™200



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ABSTRACT

RapidHIT™200 (IntegenX) is an all-in-one instrument built to produce STR profiles of reference samples (buccal swabs) in 90 min with minimal hands-on time. The aim of this study was to investigate the performance of the RapidHIT™200 with regards to analysis of buccal swabs and to explore the possibilities of employing the instrument for analysis of more challenging sample formats than buccal swabs. Mouth swabs gave 74% full STR profiles with correctly assigned alleles. Full STR profiles were obtained with dilutions of lymphocyte DNA spotted onto cotton swabs with a range of 900–1200 ng DNA. With lower and higher amounts of DNA, drop-outs of alleles and loci were observed. There was no obvious correlation between the amounts of input DNA and the peak heights of the alleles in the profiles. However, when the peak height was low, the risk of obtaining a partial profile was increased. A piece of muscle from an identification case from 2007 was thawed and rubbed with cotton swabs for 10, 20 and 40 s. The rapidHIT™200 analyses gave partial STR profiles corresponding to a degradation pattern with correctly assigned alleles. In general, STR alleles were assigned correctly and the muscle experiment was promising. There was no correlation between input DNA and peak height. The sensitivity of the RapidHIT™200 is lower than those of conventional STR typing methods.

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1. Introduction

Using a portable kit to quickly analyze human DNA collected in the field (Rapid DNA) could be advantageous in situations like disaster victim identification and rapid intelligence in crime cases. Several manufacturers have developed prototype instruments for Rapid DNA. The RapidHIT™200 (IntegenX) gives STR profiles from five buccal swabs in 90 min using the PowerPlex® 16 (Promega) as the multiplex STR kit. Employing a Rapid DNA instrument for forensic investigations requires thorough studies on reliability, reproducibility and robustness. The aim of this study was to investigate the performance of the RapidHIT™200 with regards to analysis of buccal swabs and to explore the possibilities of using the instrument for analysis of more challenging sample formats than buccal swabs.

2. Materials and methods

A total of 19 mouth swabs were collected from 11 individuals on cotton swabs. Lymphocytes were isolated from a blood sample using LymphoPrep™ (Axis-Shield PoC AS) and counted in a KX-21N automated hematology analyzer (Sysmex). Serial dilutions of the cell suspension were prepared with 6.25 ng DNA–6000 ng DNA

and were spotted onto two cotton swabs. One cotton swab was analyzed with the RapidHIT200. The other one underwent conventional DNA extraction by Chelex® (BioRad) followed by Amicon® clean up, DNA quantification by Quantifiler® Hum (LT) and DNA profile analysis (AmpF/STR® NGMSelect™, LT [1]). Muscle tissue from a partly mummified body stored at –20 °C for 6 years was thawed, and biological material was collected from the tissue by rubbing two series of cotton swabs against the tissue for 10, 20 and 40 s. One series of the cotton swabs were analyzed with the RapidHIT and the other one underwent conventional DNA extraction by Chelex® (BioRad) followed by Amicon® clean up, DNA quantification by Quantifiler® Hum (LT) and DNA profile analysis (PowerPlex 16, Promega). All RapidHIT results were analyzed with GeneMarker HID (SoftGenetics) with an analytical threshold of 50 RFU and a global cut off filter of 25%.

3. Results and discussion

Of the 19 mouth swabs, 14 gave full profiles, three gave partial profiles and two gave no results at all. All alleles were assigned correctly. The interlocus balance was poor, but this could be intrinsic to the PowerPlex 16 kit. The allelic balances of heterozygous loci in full profiles were in the range 0.5–2.3 (not shown). To explore the relationship between the amount of DNA and the profile quality, four runs with serial dilutions of lymphocytes were performed. STR-profiles were obtained with samples with 300–3000 ng DNA. Full STR-profiles were obtained

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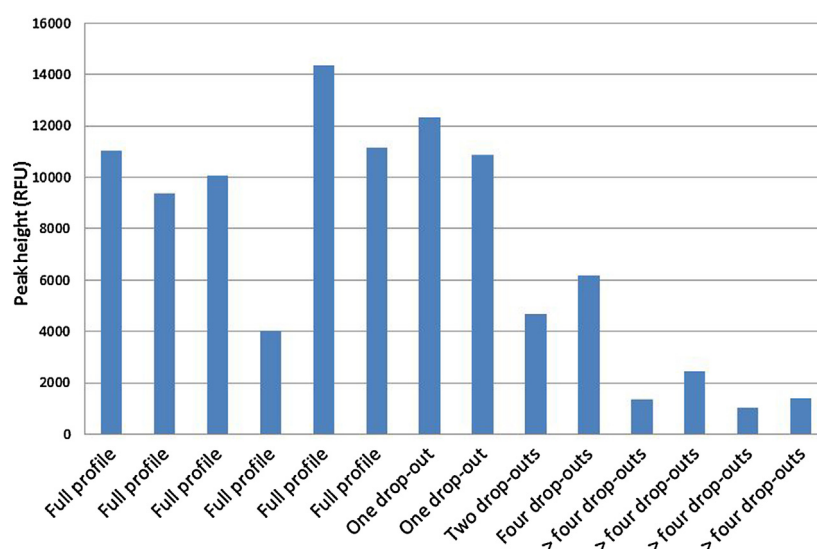


Fig. 1. Peak heights of STR profiles from lymphocytes.

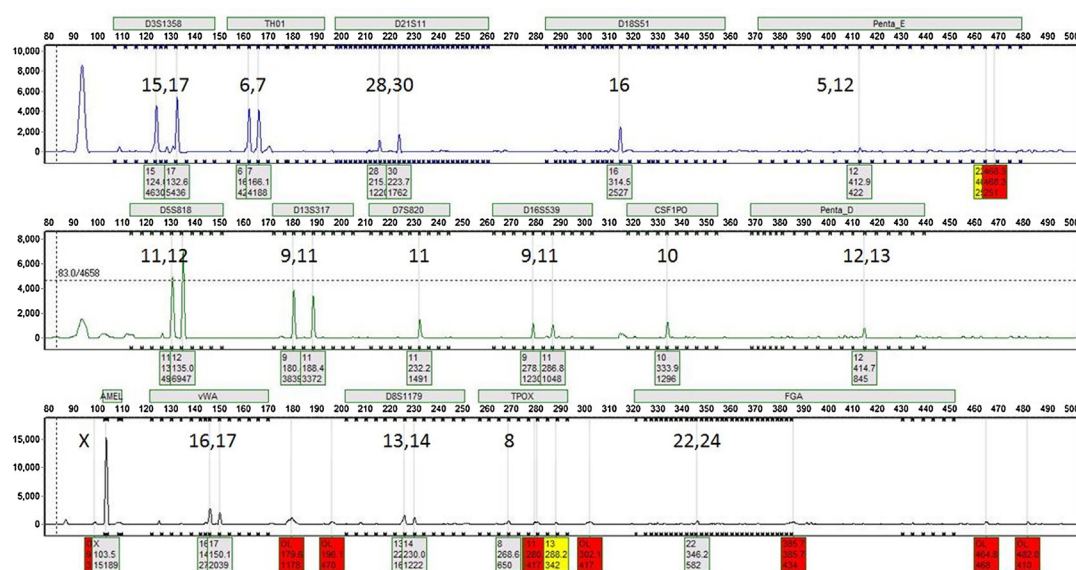


Fig. 2. Electropherogram of STR profile from muscle.

only in the range 900–1200 ng DNA. There was no obvious correlation between peak heights and DNA amounts (not shown). However, when STR-profiles were partial, the peak heights were low (Fig. 1).

Rubbing muscle tissue for 10, 20 and 40 s gave DNA yields of 75–150 ng DNA when extracted with Chelex[®]. The three samples gave very partial profiles. The 20 s sample gave the best results (Fig. 2). All alleles were assigned correctly.

4. Conclusion

The RapidHIT[™]200 in the tested version is a promising tool for DNA profile analysis of reference samples in the field. It required a minimum of hands-on time and was very easy to operate. However, only STR loci included in PowerPlex 16 STR, which we do not use in routine work, could be investigated. DNA from mouth swabs gave 74% correct STR profiles. The current version demands large amounts of DNA to produce full profiles (900–1200 ng). The balance of signals between loci and between alleles of the same loci

was poor. Thus, it is a question if the current version of RapidHIT[™]200 is suitable for analysis of reference samples with low amounts of DNA and other simple biological material like swabbed muscle tissue.

Role of funding

None.

Conflict of interest

None.

Reference

- [1] T. Tvedebrink, H.S. Mogensen, M.S. Stene, N. Morling, Performance of two 17 locus forensic identification STR kits - Applied Biosystems's AmpFISTR[®] NGMSelect[™] and Promega's PowerPlex[®] ESI17 kits, *Forensic Sci. Int. Genet.* 6 (2012) 523–533., <http://dx.doi.org/10.1016/j.fsigen.2011.12.006>.